Amendments to the Specification:

Please amend the specification as follows:

Please replace paragraph [0009] with the following rewritten paragraph:

The recombinase specific of said SSRTS is selected from the group of site-specific recombinases composed of the Cre recombinase of bacteriophage P1, the FLP recombinase of *Saccharomyces cerevisiae*, the R recombinase of *Zygosaccharomyces rouxii* pSR1, the A recombinase of Kluyveromyces drosophilarium pKD1, the A recombinase of *Kluyveromyces waltii* pKW1, the integrase λInt, the recombinase of the GIN recombination system of the Mu phage, of the bacterial β recombinase or a variant thereof. In a preferred embodiment, the recombinase is the Cre recombinase of bacteriophage P1 (Abremski et al., 1984), or its natural or synthetic variants. Cre is available commercially (Novagen, Catalog No. 69247-1). Recombination mediated by Cre is freely reversible. Cre works in simple buffers with either magnesium or spermidine as a cofactor, as is well known in the art. The DNA substrates can be either linear or supercoiled. A number of mutant loxP sites have been described (Hoess et al., 1986; Lee et al., 1998), indeed, the corresponding SSRTS L1 and/or L2 specific for said Cre recombinase are chosen from the group composed of the sequences Lox P1 (ATCC 53 254 et 20 773), Lox 66, Lox 71, Lox 511, Lox 512, Lox 514, Lox B, Lox L, Lox R and mutated sequences of Lox P1 site harboring at least one point mutation in the 8 nucleotide spacer sequence. In one embodiment, the point mutation is substitution of A for G at position 7 of the eight base spacer sequence of the wild type Lox P1 sequence, referred to herein as the Lox511 sequence. Preferred SSRTS are Lox P1 (SEQ ID N° [[1]] 52) and Lox 511 (SEQ ID N° 53).

Please replace paragraph [0075] with the following rewritten paragraph:

3' RACE was carried out as described by Frohman (1994). Briefly, a first RT-PCR was carried out using the oligonucleotides Qt (5'-CCAGTGAGCAGAGTGACG AGGACTCGAGCTCAAGCT17-3') (SEQ ID N° 47) as anchor primer, as well as Q0 (5'-CCAGTGAGCAGAGTGACG-3') (SEQ ID N° 48) and Neo1 (3'-ACCGCTTCCTCGTGCTTTAC-3') (SEQ ID N° 49) for amplification. An aliquot of 1 µl of

this reaction was used for a nested amplification using Q1 (5'-GAGGACTCGAGCTCAAGC-3') (SEQ ID N° 50) and Neo2 (5'-GCCTTCTTGACGAGTTCTTC-3') (SEQ ID N° 51) primers. The resulting PCR fragments were purified using the NucleoSpin kit (Macherey-Nagel) and sequenced using the Neo2 or OBS (5'-CTGTAAAACGACGGCCAGTC-3') (SEQ ID N° [[52]] 57) primers.

Please replace the sequence listing starting after paragraph [0165] and before the claims with the amended sequences listing submitted herewith.